

What is claimed is:

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1. A method for determining whether a test plant has been exposed to an abiotic stress condition, the method comprising contacting nucleic acid molecules representative of expressed polynucleotides in cells of the test plant with at least one nucleic acid probe under conditions suitable for selective hybridization to a complementary nucleotide sequence,

wherein the probe comprises at least 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:1-155, 157-228, 230-232, 234-557, 559-572, 574-605, 607-634, 636-786, 788-812, 814-1261, 2227-2585, 2704-2857-2928, 2930-2932, 2934-3256, 3258-3271, 3273-3304, 3306-3323, 3325-3333, 3335-3485, 3487-3511, 3313-3955, and 4910-5263, or a nucleotide sequence complementary thereto,

whereby

detecting selective hybridization of at least one nucleic acid probe, or
detecting a change in a level of selective hybridization as compared to
a level of selective hybridization obtained using nucleic acid molecules
representative of expressed polynucleotides in cells of a plant known not have
been exposed to an abiotic stress,

indicates that the test plant has been exposed to an abiotic stress
condition, and

whereby an absence of selective hybridization of at least one nucleic acid
probe indicates that the test plant has not been exposed to an abiotic stress condition.

2. The method of claim 1, wherein the abiotic stress is cold stress, and
wherein the probe comprises at least 15 nucleotides of a nucleotide sequence as set
forth in any of SEQ ID NOS:1-155, 157-228, 230-232, 234-557, 559-572, 574-605,
607-634, 636-786, 788-812, 814-1261, 2704-2857-2928, 2930-2932, 2934-3256,
3258-3271, 3273-3304, 3306-3323, 3325-3333, 3335-3485, 3487-3511, and 3313-
3955, or a nucleotide sequence complementary thereto.

3. The method of claim 1, wherein the abiotic stress is saline stress, and wherein the probe comprises at least 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:2226-2427 or a nucleotide sequence complementary thereto.

4. The method of claim 1, wherein the abiotic stress is osmotic stress, and wherein the probe comprises at least 15 nucleotides of a nucleotide sequence as set forth in two or more of SEQ ID NOS:2428-2585 or a nucleotide sequence complementary thereto.

5. A method for determining whether a test plant has been exposed to a combination of abiotic stress conditions, the method comprising contacting nucleic acid molecules representative of expressed polynucleotides in cells of the test plant with at least one nucleic acid probe under conditions suitable for selective hybridization to a complementary nucleotide sequence,

wherein the probe comprises at least 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:1262-2226, 2586-2703, 3956-4909, and 5264-5379, or a nucleotide sequence complementary thereto,

whereby

detecting selective hybridization of at least one nucleic acid probe, or

detecting a change in a level of selective hybridization as compared to a level of selective hybridization obtained using nucleic acid molecules representative of expressed polynucleotides in cells of a plant known not have been exposed to a combination of stress conditions,

indicates that the test plant has been exposed to a combination of abiotic stress conditions, and

whereby an absence of selective hybridization of at least one nucleic acid probe indicates that the test plant has not been exposed to a combination of abiotic stress conditions.

6. The method of claim 5, wherein the combination of abiotic stress conditions is a combination of a cold stress and an osmotic stress, and wherein the probe comprises at least 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:1699-1969, or a nucleotide sequence complementary thereto.

7. The method of claim 5, wherein the combination of abiotic stress conditions is a combination of a cold stress and an osmotic stress, and wherein the probe comprises at least 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:1699-1725, 1727-1865, 1867-1917, 1919-1927, 1929-1969, 4389-4414, 4416-4552, 4554-4602, and 4604-4654, or a nucleotide sequence complementary thereto.

8. The method of claim 5, wherein the combination of abiotic stress conditions is a combination of a cold stress and a saline stress, and wherein the probe comprises at least 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:1970-2226 and 4655-4909, or a nucleotide sequence complementary thereto.

9. The method of claim 5, wherein the combination of abiotic stress conditions is a combination of an osmotic stress and a saline stress, and wherein the probe comprises at least 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:2586-2703 and 5264-5379, or a nucleotide sequence complementary thereto.

10. The method of claim 5, wherein the combination of abiotic stress conditions is a combination of a cold stress, a saline stress and an osmotic stress, and wherein the probe comprises at least 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:1262-1698, or a nucleotide sequence complementary thereto.

11. The method of claim 5, wherein the combination of abiotic stress conditions is a combination of a cold stress, a saline stress and an osmotic stress, and wherein the probe comprises at least 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:1262, 1264-1386, 1387-1390, 1392-1404, 1406-1444, 1446-1483, 1485-1588, 1590-1608, 1610-1633, 1635-1698, 3956, 3958-4078, 4080-4097, 4099-4136, 4138-4175, 4177-4279, 4281-4299, 4301-4324, 4326-4388, or a nucleotide sequence complementary thereto.

12. A method for determining whether a test plant has been exposed to an abiotic stress condition or combination of abiotic stress conditions, the method comprising detecting a level of expression of at least one polynucleotide comprising a nucleotide sequence as set forth in any of SEQ ID NOS:1-155, 157-228, 230-232, 234-557, 559-572, 574-605, 607-634, 636-786, 788-812, 814-1262, 1264-1386, 1387-1390, 1392-1404, 1406-1444, 1446-1483, 1485-1588, 1590-1608, 1610-1633, 1634-1725, 1727-1865, 1867-1917, 1919-1927, 1929-2855, 2857-2928, 2930-2932, 2934-3256, 3258-3271, 3273-3304, 3306-3323, 3325-3333, 3335-3485, 3487-3511, 3313-3956, 3958-4078, 4080-4097, 4099-4136, 4138-4175, 4177-4279, 4281-4299, 4301-4324, 4326-4414, 4416-4552, 4554-4602, and 4604-5379, in cells of the test plant, wherein

detecting a level of expression that is at least about two-fold different from a level of expression of the at least one polynucleotide in cells of a plant not exposed to an abiotic stress or combination of abiotic stresses, or

detecting a level of expression that is less than about two-fold different from a level of expression of the at least one polynucleotide in cells of a plant known to be exposed to an abiotic stress or combination of abiotic stresses,

indicates the test plant has been exposed to an abiotic stress or combination of abiotic stresses, or

wherein

detecting a level of expression that is less than at least about two-fold different from a level of expression of the at least one polynucleotide in cells of a plant not exposed to an abiotic stress or combination of abiotic stresses, or

detecting a level of expression that is at least two-fold different from a level of expression of the at least one polynucleotide in cells of a plant known to be exposed to an abiotic stress or combination of abiotic stresses,

indicates the test plant has not been exposed to an abiotic stress or combination of abiotic stresses.

13. The method of claim 12, wherein the abiotic stress condition is a cold stress, the method comprising detecting a level of expression of at least one polynucleotide comprising a nucleotide sequence as set forth in SEQ ID NOS:1-155, 157-229, 230-232, 234-557, 559-572, 574-605, 607-634, 636-634, 636-786, 788-812, and 814-1261 in cells of the test plant.

14. The method of claim 12, wherein the abiotic stress condition is a saline stress, the method comprising detecting a level of expression of at least one polynucleotide comprising a nucleotide sequence as set forth in SEQ ID NOS:2226-2427 in cells of the test plant.

15. The method of claim 12, wherein the abiotic stress condition is an osmotic stress, the method comprising detecting a level of expression of at least one polynucleotide comprising a nucleotide sequence as set forth in SEQ ID NOS:2428-2585 in cells of the test plant.

16. The method of claim 12, wherein the combination of abiotic stress conditions is a cold stress and an osmotic stress, the method comprising detecting a level of expression of at least one polynucleotide comprising a nucleotide sequence as set forth in SEQ ID NOS:1699-1725, 1727-1865, 1867-1917, 1919-1927, 1929-1969, 4389-4414, 4416-4552, 4554-4602, and 4604-4654 in cells of the test plant.

17. The method of claim 12, wherein the combination of abiotic stress conditions is a cold stress and a saline stress, the method comprising detecting a level of expression of at least one polynucleotide comprising a nucleotide sequence as set forth in SEQ ID NOS:1970-2226 in cells of the test plant.

18. The method of claim 12, wherein the combination of abiotic stress conditions is a saline stress and an osmotic stress, the method comprising detecting a level of expression of at least one polynucleotide comprising a nucleotide sequence as set forth in SEQ ID NOS:2586-2703 in cells of the test plant.

19. The method of claim 12, wherein the combination of abiotic stress conditions is a combination of a cold stress, a saline stress and an osmotic stress, the method comprising detecting a level of expression of at least one polynucleotide comprising a nucleotide sequence as set forth in any of SEQ ID NOS:1262, 1264-1386, 1387-1390, 1392-1404, 1406-1444, 1446-1483, 1485-1588, 1590-1608, 1610-1633, 1635-1698, 3956, 3958-4078, 4080-4097, 4099-4136, 4138-4175, 4177-4279, 4281-4299, 4301-4324, 4326-4388, or a nucleotide sequence complementary thereto.

20. A method of identifying a stress condition to which a plant cell has been exposed, the method comprising:

- a) contacting nucleic acid molecules representative of expressed polynucleotides in the plant cell with an array of probes representative of the plant cell genome; and
- b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response, thereby identifying the stress condition to which the plant cell was exposed.

21. The method of claim 20, wherein the stress condition is an abiotic stress condition.

22. The method of claim 21, wherein the abiotic stress is a cold stress condition, an osmotic stress condition, a saline stress condition, or a combination thereof.

23. The method of claim 20, wherein the profile is characteristic of exposure to a single stress condition.

24. The method of claim 23, wherein the profile is selected from
- a profile characteristic of a cold stress response, and wherein the expressed polynucleotides comprise one or a plurality of SEQ ID NOS:1-155, 157-229, 230-232, 234-557, 559-572, 574-605, 607-634, 636-634, 636-786, 788-812, and 814-1261;
 - a profile characteristic of a cold stress response, and wherein the expressed polynucleotides comprise one or a plurality of SEQ ID NOS:1-1261;
 - a profile is characteristic of an osmotic stress response, and wherein the expressed polynucleotides comprise one or a plurality of SEQ ID NOS:2428-2585;

a profile is characteristic of a saline stress response, and wherein the expressed polynucleotides comprise one or a plurality of SEQ ID NOS:2227-2427.

25. The method of claim 20, wherein the profile is characteristic of exposure to a combination of stress conditions.

26. The method of claim 25, wherein the combination of abiotic stress conditions are selected from

a cold stress and an osmotic stress, and wherein the expressed polynucleotides comprise one or a plurality of SEQ ID NOS:1699-1725, 1727-1865, 1867-1917, 1919-1927, and 1929-1969;

a cold stress and an osmotic stress, and wherein the expressed polynucleotides comprise one or a plurality of SEQ ID NOS:1699-1969;

a cold stress and a saline stress, and wherein the expressed polynucleotides comprise one or a plurality of SEQ ID NOS:1970-2226;

an osmotic stress and a saline stress, and wherein the expressed polynucleotides comprise one or a plurality of SEQ ID NOS:2586-2703;

a cold stress, an osmotic stress, and a saline stress, and wherein the expressed polynucleotides comprise one or a plurality of SEQ ID NOS:1262, 1264-1386, 1387-1390, 1392-1404, 1406-1444, 1446-1483, 1485-1588, 1590-1608, 1610-1633, and 1634-1698; and

a cold stress, an osmotic stress, and a saline stress, and wherein the expressed polynucleotides comprise one or a plurality of SEQ ID NOS:1262-1698.

27. The method of claim 20, wherein the nucleic acid molecules representative of expressed polynucleotides in the plant cell are RNA molecules or cDNA molecules.

28. The method of claim 20, wherein the array of probes representative of the plant cell genome is immobilized on a microchip.

29. A method of producing a transgenic plant comprising plant cells that exhibit altered responsiveness to at least one stress condition, the method comprising introducing a polynucleotide portion of a plant stress-regulated gene into a plant cell genome, wherein the polynucleotide portion of the stress-regulated gene comprises a nucleotide sequence as set forth in any of 1-155, 157-228, 230-232, 234-557, 559-572, 574-605, 607-634, 636-786, 788-812, 814-1262, 1264-1386, 1387-1390, 1392-1404, 1406-1444, 1446-1483, 1485-1588, 1590-1608, 1610-1633, 1634-1725, 1727-1865, 1867-1917, 1919-1927, 1929-2855, 2857-2928, 2930-2932, 2934-3256, 3258-3271, 3273-3304, 3306-3323, 3325-3333, 3335-3485, 3487-3511, 3313-3956, 3958-4078, 4080-4097, 4099-4136, 4138-4175, 4177-4279, 4281-4299, 4301-4324, 4326-4414, 4416-4552, 4554-4602, and 4604-5379, whereby the polynucleotide portion of the plant stress-regulated gene modulates a response of the plant cells to at least one stress condition, thereby producing a transgenic plant comprising plant cells that exhibit altered responsiveness to the stress condition.

30. The method of claim 29, wherein the transgenic plant comprises plant cells that exhibit altered responsiveness to a combination of a combination of at least two stress conditions.

31. The method of claim 30, wherein the combination of at least two stress conditions is a combination of

cold stress and osmotic stress, and wherein the polynucleotide portion of the plant stress-regulate gene comprises a nucleotide sequences as set forth in any of SEQ ID NOS:1669-1969 and 4389-4654;

cold stress and osmotic stress, and wherein the polynucleotide portion of the plant stress-regulate gene comprises a nucleotide sequences as set forth in any of SEQ ID NOS:1699-1725, 1727-1865, 1867-1917, 1919-1927,

1929-1969, 4389-4414, 4416-4552, 4554-4602, 4604-4612, and 4613-4654;
cold stress and saline stress, and wherein the polynucleotide portion of
the plant stress-regulate gene comprises a nucleotide sequences as set forth in
any of SEQ ID NOS:1970-2226 and 4655-4909;

osmotic stress and saline stress, and wherein the polynucleotide portion
of the plant stress-regulate gene comprises a nucleotide sequences as set forth in
any of SEQ ID NOS:2586-2703 and 5264-5379;

cold stress, osmotic stress and saline stress, and wherein the
polynucleotide portion of the plant stress-regulate gene comprises a nucleotide
sequences as set forth in any of SEQ ID NOS:1262-1698 and 3956-4388; or

cold stress, osmotic stress and saline stress, and wherein the
polynucleotide portion of the plant stress-regulate gene comprises a nucleotide
sequences as set forth in any of SEQ ID NOS:1262, 1264-1386, 1387-1390,
1392-1404, 1406-1444, 1446-1483, 1485-1588, 1590-1608, 1610-1633,
1634-1698, 3956, 3958-4078, 4080-4097, 4099-4136, 4138-4175, 4177-4279,
4281-4299, 4301-4324, and 4326-4388.

32. The method of claim 29, wherein the polynucleotide portion of the plant
stress-regulated gene encodes a stress-regulated polypeptide or functional peptide
portion thereof.

33. The method of claim 32, wherein the stress-regulated polypeptide or
functional peptide portion thereof increases the stress tolerance of the transgenic
plant.

34. The method of claim 32, wherein the stress-regulated polypeptide or
functional peptide portion thereof decreases the stress tolerance of the transgenic
plant.

35. The method of claim 32, wherein the polynucleotide portion of the plant stress-regulated gene is operatively linked to a heterologous promoter.

36. The method of claim 29, wherein the polynucleotide portion of the plant stress-regulated gene comprises a stress-regulated regulatory element.

37. The method of claim 36, wherein, upon introducing the stress-regulated regulatory element into the plant cell, the regulatory element integrates into the plant cell genome in a site-specific manner.

38. The method of claim 37, wherein, upon integrating into the plant cell genome, the regulatory element is operatively linked to a heterologous nucleotide sequence, which can be expressed in response to a stress condition specific for the regulatory element.

39. The method of claim 36, wherein the plant stress-regulated regulatory element is a mutant regulatory element, which is not responsive to the stress condition, whereby upon integrating into the plant cell genome, the mutant regulatory element disrupts an endogenous stress-regulated regulatory element of a plant stress-regulated gene, thereby altering the responsiveness of the plant stress-regulated gene to the stress condition.

40. The method of claim 29, wherein the stress is an abiotic stress.

41. The method of claim 36, wherein the stress-regulated regulatory element is operatively linked to a polynucleotide encoding a detectable marker.

42. A transgenic plant produced by the method of claim 29.

43. A plant cell from the transgenic plant of claim 42, wherein said plant cell exhibits altered responsiveness to the stress condition or stress conditions.

44. A seed produced by the transgenic plant of claim 42.

45. A cDNA or genomic DNA library prepared from the transgenic plant of claim 42, or from a plant cell from said transgenic plant, wherein said plant cell exhibits altered responsiveness to the stress condition.

46. A transgenic plant, which contains a transgene comprising a polynucleotide portion of plant stress-regulated gene, wherein the gene comprises a nucleotide sequence as set forth in any of SEQ ID NOS:1-155, 157-228, 230-232, 234-557, 559-572, 574-605, 607-634, 636-786, 788-812, 814-1262, 1264-1386, 1387-1390, 1392-1404, 1406-1444, 1446-1483, 1485-1588, 1590-1608, 1610-1633, 1634-1725, 1727-1865, 1867-1917, 1919-1927, 1929-2855, 2857-2928, 2930-2932, 2934-3256, 3258-3271, 3273-3304, 3306-3323, 3325-3333, 3335-3485, 3487-3511, 3313-3956, 3958-4078, 4080-4097, 4099-4136, 4138-4175, 4177-4279, 4281-4299, 4301-4324, 4326-4414, 4416-4552, 4554-4602, and 4604-5379.

47. The transgenic plant of claim 46, wherein the transgenic plant exhibits altered responsiveness to a stress condition as compared to a corresponding wild-type plant.

48. The transgenic plant of claim 47, wherein the transgene disrupts an endogenous stress-regulated gene in the plant, thereby reducing or inhibiting expression of the gene in response to a stress condition.

49. The transgenic plant of claim 46, wherein the plant exhibits increased tolerance to a stress condition.

50. The transgenic plant of claim 47, wherein the plant exhibits decreased tolerance to a stress condition.

51. The transgenic plant of claim 46, wherein the transgene comprises a coding sequence of a plant stress-regulated gene.

52. The transgenic plant of claim 51, wherein the coding sequence is operatively linked to a heterologous regulatory element.

53. The transgenic plant of claim 52, wherein the regulatory element is a constitutively active regulatory element, an inducible regulatory element, or a tissue specific or phase specific regulatory element.

54. The transgenic plant of claim 46, wherein the transgene comprises a plant stress-regulated regulatory element operatively linked to a heterologous nucleotide sequence.

55. The transgenic plant of claim 54, wherein the transgenic plant expresses a polypeptide encoded by the heterologous nucleotide sequence.

56. The transgenic plant of claim 55, wherein the polypeptide improves the nutritional value or ornamental value of the plant.

57. The transgenic plant of claim 46, wherein the plant comprises multiple transgenes.

58. A plant stress-regulated gene regulatory element, wherein the gene comprises a nucleotide sequence as set forth in any of SEQ ID NOS:1-155, 157-228, 230-232, 234-557, 559-572, 574-605, 607-634, 636-786, 788-812, 814-1262, 1264-1386, 1387-1390, 1392-1404, 1406-1444, 1446-1483, 1485-1588, 1590-1608, 1610-1633, 1634-1725, 1727-1865, 1867-1917, 1919-1927, 1929-2855, 2857-2928, 2930-2932, 2934-3256, 3258-3271, 3273-3304, 3306-3323, 3325-3333, 3335-3485, 3487-3511, 3513-3956, 3958-4078, 4080-4097, 4099-4136, 4138-4175, 4177-4279, 4281-4299, 4301-4324, 4326-4414, 4416-4552, 4554-4602, and 4604-5379.

59. The plant stress-regulated gene regulatory element of claim 144, comprising a nucleotide sequence as set forth in any of SEQ ID NOS:2704-2855, 2857-2928, 2930-2932, 2934-3256, 3258-3304, 3306-3323, 3325-3333, 3335-3485, 3487-3511, 3513-3956, 3958-4078, 4080-4097, 4099-4136, 4138-4175, 4177-4279,, 4281-4299, 4301-4324, 4326-4414, 4416-4552, 4554-4602, 4604-4612, and 4614-5379.

60. A method for monitoring a population of plants for exposure to a stress condition or combination of stress conditions, the method comprising:

a) introducing into the population of a plants a sentinel plant, wherein said sentinel plant is a transgenic plant of claim 46, which comprises plant cells containing a stress-regulated gene regulatory element is operatively linked to a polynucleotide encoding a detectable marker,

wherein the stress-regulated gene regulatory element comprises a nucleotide sequence as set forth in any of SEQ ID NOS:2704-2855, 2857-2928, 2930-2932, 2934-3256, 3258-3304, 3306-3323, 3325-3333, 3335-3485, 3487-3511, 3513-3956, 3958-4078, 4080-4097, 4099-4136, 4138-4175, 4177-4279,, 4281-4299, 4301-4324, 4326-4414, 4416-4552, 4554-4602, 4604-4612, and 4614-5379; and

b) examining the sentinel plant for expression of the detectable marker, which is indicative of exposure of the population of plants to a stress condition or combination of stress conditions, thereby monitoring the population of plants for exposure to a stress condition or combination of stress conditions.

61. The method of claim 60, wherein said stress condition or combination of stress conditions is an abiotic stress condition or combination of abiotic stress conditions.

62. The method of claim 60, wherein the detectable marker is visibly detectable.

63. The method of claim 60, wherein said detectable marker comprises a luminescent detectable marker.

64. The method of claim 60, wherein said detectable marker comprises a fluorescent detectable marker.

65. The method of claim 64, wherein said fluorescent detectable marker comprises a green fluorescent protein, a yellow fluorescent protein, a cyan fluorescent protein, a red fluorescent protein, or an enhanced or modified form thereof.

66. A method of selecting a plant having an altered resistance to an abiotic stress condition or a combination of abiotic stress conditions, the method comprising:

a) contacting nucleic acid molecules representative of expressed polynucleotides in a plant cell of a plant to be examined for having an altered resistance to an abiotic stress with a nucleic acid probe that selectively hybridizes under stringent conditions to a plant stress-regulated gene comprising a nucleotide sequence as set forth in any of SEQ ID NO:1-155,

157-228, 230-232, 234-557, 559-572, 574-605, 607-634, 636-786, 788-812, 814-1262, 1264-1386, 1387-1390, 1392-1404, 1406-1444, 1446-1483, 1485-1588, 1590-1608, 1610-1633, 1634-1725, 1727-1865, 1867-1917, 1919-1927, 1929-2855, 2857-2928, 2930-2932, 2934-3256, 3258-3271, 3273-3304, 3306-3323, 3325-3333, 3335-3485, 3487-3511, 3313-3956, 3958-4078, 4080-4097, 4099-4136, 4138-4175, 4177-4279, 4281-4299, 4301-4324, 4326-4414, 4416-4552, 4554-4602, and 4604-5379;

b) detecting a level of selective hybridization of the nucleic acid probes to a nucleic acid molecule representative of an expressed polynucleotide in the plant cell, wherein the level of selective hybridization corresponds to the level of the expressed polynucleotide in the plant cell, which is indicative of resistance of the plant to an abiotic stress; and

c) selecting a plant having a level of expression of a polynucleotide indicative of altered resistance to an abiotic stress condition.

67. A method of expressing a heterologous nucleotide sequence in a plant cell, the method comprising introducing into the plant cell a plant stress-regulated regulatory element of claim 58 operatively linked to the heterologous nucleotide sequence, whereby, upon exposure of the plant cell to stress condition, the heterologous nucleotide sequence is expressed in the plant cell.

68. The method of claim 67, wherein the heterologous nucleotide sequence encodes a selectable marker.

69. The method of claim 67, wherein the heterologous nucleotide sequence encodes a polypeptide that improves the nutritional value of the plant cell.

70. The method of claim 67, wherein the heterologous nucleotide sequence encodes a polypeptide that improves the ornamental value of the plant cell.

71. A method of identifying an agent that modulates the activity of a plant stress-regulated gene regulatory element, the method comprising:

- a) contacting a plant stress-regulated gene regulatory element of claim 58 with an agent suspected of having the ability to modulate the activity of the regulatory element; and
- b) detecting a change in the activity of the regulatory element, thereby identifying an agent that modulates the activity of the plant stress-regulated regulatory element.

72. The method of claim 71, wherein the regulatory element can be operatively linked to a heterologous nucleotide sequence.

73. The method of claim 72, wherein the heterologous nucleotide sequence encodes a reporter molecule.

74. The method of claim 7, which is performed *in vitro* in a plant cell-free system, in a plant cell in culture, or in a plant *in situ*.

75. A method for identifying a polynucleotide involved in a stress response of a plant, the method comprising:

- a) contacting nucleic acid molecules representative of expressed polynucleotides in plant cells of a plant exposed to a stress condition or combination of stress conditions with an array of probes representative of the plant cell genome; and
- b) detecting a nucleic acid molecule that exhibits at least a two-fold change in the level of expression as compared to the level of the nucleic acid molecule in a corresponding plant cell of a plant that was not exposed to the stress condition, thereby identifying a polynucleotide involved in a stress response of the plant.



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76. The method of claim 75, comprising identifying a plurality of polynucleotides involved in the stress response in the plant.

77. The method of claim 75, further comprising isolating the polynucleotide or plurality of polynucleotides.

78. A computer readable medium having stored thereon computer executable instructions for performing a method comprising:

- a) receiving data on expression in a cell of a plant of a nucleic acid molecule having at least 70% sequence identity to a nucleotide sequence comprising any of SEQ ID NO. 1-5379; and
- b) comparing the data on expression of the nucleic acid molecule with data on expression of the nucleic acid in a cell of a plant that has not been exposed to an abiotic stress, of a plant that has been exposed to an abiotic stress condition or combination of abiotic stress conditions, or of a combination of such plants.

79. A computer-readable medium having stored thereon a data structure comprising:

sequence data for at least one nucleic acid molecule having at least 70% nucleic acid sequence identity to a polynucleotide having a nucleotide sequence as set forth in any of SEQ ID NO. 1-5379 or a nucleotide sequence complementary thereto; and

a module receiving the nucleic acid molecule sequence data, which compares the nucleic acid molecule sequence data to a least one other nucleic acid sequence.